A1 Provisional Application 60/075,979, filed February 25, 1998 and U.S. Provisional Application 60/106,038, filed October 28, 1998.

Please replace the paragraph beginning at page 8, line 26, with the following rewritten paragraph:

A2 FIG. 26A is a schematic diagram of a breast cancer tissue microarray, as well as a digital image of a hybridization, showing that FGFR2 was amplified in 4.5% of the tumor samples in the breast cancer tissue microarray. FIG. 26B is an enlargement of a single donor specimen in the breast cancer tissue microarray.

In the claims:

Please amend the claims as follows:

A3 1. (Amended) A method of parallel analysis of biological specimens, comprising:

obtaining a plurality of donor specimens;

placing each donor specimen in an assigned location in a recipient array;

obtaining a plurality of substantial copies of the recipient array in a manner that each substantial copy contains a plurality of donor specimens that maintain their assigned locations;

performing a biological analysis of each substantial copy; and

comparing the results of the biological analysis in corresponding assigned locations of different substantial copies to determine if there are correlations between the results of the biological analysis at each assigned location.

A4 9. (Amended) The method of claim 1, further comprising associating a clinical characteristic with each assigned location in the recipient array.

A5 12. (Amended) The method of claim 10, further comprising determining whether there are correlations between clinical characteristics, associated with each assigned location, and the different biological analyses.

14. (Amended) The method of claim 12, wherein the clinical characteristics are determined apart from performing the different biological analysis of each copy of the array; and

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the characteristics are one or more of patient age, tumor grade, tumor size, node status, and receptor status.

16. (Amended) A method of parallel analysis of substantially identical arrays of tissue specimens, comprising:

forming a donor block comprising a biological specimen embedded in embedding medium;

obtaining a plurality of elongated donor sample cores from the biological specimen;

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boring receptacle cores from a recipient embedding medium to form an array of elongated receptacles;

placing the donor sample cores in the elongated receptacles at assigned locations in the array;

sectioning the recipient embedding medium transverse to the elongated receptacles to obtain a cross-section of the donor sample cores in the array, while maintaining the assigned locations in the array in consecutive cross-sections;

performing a different biological analysis of each cross-section; and

comparing a result of each biological analysis in corresponding assigned locations of different sections to determine if there are correlations between the results of the different biological analyses at each assigned location.

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23. (Amended) A cross-section of the donor sample cores obtained by the method of claim 16.

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24 25. (Amended) The method of claim 24, wherein the nucleic acid microarray is a cDNA or oligonucleotide microarray.

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42 43. (Amended) The method of claim 1, further comprising analyzing the results of the biological analyses to:

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a. evaluate a reagent for disease diagnosis or treatment;

b. identify a prognostic marker for a disease;

c. prioritize targets for drug development;

d. assess or select therapy for a disease type;

e. find a biochemical target for medical therapy;

f. determine the frequency of a target in pathological and normal physiological tissue;

g. identify therapeutic targets that are expressed in pathological tissue relative to normal physiological tissue;

h. compare the expression or presence of a target at the DNA, RNA and protein level; or

i. identify, validate, and prioritize targets that are defined by utilizing bioinformatic analyses.

~~49~~ 50. (Amended) The method of claim ~~49~~ 48, wherein the donor specimens are from breast cancer tumors.

Please add the following new claims:

~~78~~ 86. (New) The method of claim ~~49~~ 48, wherein the donor specimens are specimens from one or more tumors selected from the group of prostate and bladder cancer.

~~79~~ 87. (New) The method of claim 1, wherein the method does not destroy the morphology or cellular structure of the donor specimens.

~~80~~ 88. (New) A method of parallel analysis of biological specimens, comprising:

obtaining a plurality of donor specimens;

placing each donor specimen in an assigned location in a recipient array;

obtaining a plurality of sections of the recipient array in a manner that each section contains a plurality of donor specimens that maintain their assigned locations;

performing a biological analysis of each section; and

comparing the results of the biological analysis in corresponding assigned locations of different sections to determine if there are correlations between the results of the biological analysis at each assigned location.

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81 89. (New) The method of claim 1, further comprising correlating additional information concerning the donor specimens with the biological analysis correlation, wherein the additional information is at least one of patient demographics, clinical tumor staging data, and patient follow-up data.

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82 90. (New) A method of analysis of biological specimens, comprising:

forming at least one donor block comprising a biological specimen embedded in embedding medium;

obtaining a plurality of elongated donor sample cores from the biological specimen;

boring receptacle cores from a recipient embedding medium to form an array of elongated receptacles;

placing the donor sample cores in the elongated receptacles at assigned locations in the array;

sectioning the recipient embedding medium transverse to the elongated receptacles to obtain at least one cross-section of the donor sample cores in the array, while maintaining the assigned locations in the array in consecutive cross-sections;

performing a biological analysis of each cross-section; and

analyzing the results of the biological analysis to determine the frequency of a substance of interest in the cross-sections of the donor sample cores.

83 91. (New) The method of claim 1, further comprising obtaining the donor specimens from a predetermined morphologically defined region of a tumor.

84 92. (New) The method of claim 1, further comprising obtaining the donor specimens from a predetermined cell structure.

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